

A5

#6 PCT09

## RAW SEQUENCE LISTING

DATE: 12/19/2001

PATENT APPLICATION: US/09/889,733

TIME: 15:54:47

Input Set : A:\SEQ LIST.txt

Output Set: N:\CRF3\12192001\I889733.raw

ENTERED

3 <110> APPLICANT: UNIVERSITY COLLEGE LONDON  
 5 <120> TITLE OF INVENTION: DIMETHYLARGININE DIMETHYLAMINOHYDROLASES (as amended)  
 7 <130> FILE REFERENCE: 117-358  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/889,733  
 C--> 10 <141> CURRENT FILING DATE: 2001-11-19  
 12 <150> PRIOR APPLICATION NUMBER: GB 9901705.5  
 13 <151> PRIOR FILING DATE: 1999-01-26  
 15 <150> PRIOR APPLICATION NUMBER: GB 9913066.8  
 16 <151> PRIOR FILING DATE: 1999-06-04  
 18 <160> NUMBER OF SEQ ID NOS: 13  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 858  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: H. Sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(858)  
 31 <400> SEQUENCE: 1  
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 33 Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala  
 34 1 5 10 15  
 36 gtg gtg cgg gcg cta ccc gag tcg ctc tgc cag cac gcg ctg aga agc 96  
 37 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser  
 38 20 25 30  
 40 gcc aag ggc gag gag gtg gac gtc gcc cgc gcg gaa cgg cag cac cag 144  
 41 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln  
 42 35 40 45  
 44 ctc tac gtg ggc gtg ctg ggc agc aag ctg ggg ctg cag gtg gtg gag 192  
 45 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu  
 46 50 55 60  
 48 ctg ccg gcc gac gag agc ctt ccg gac tgc gtc ttc gtg gag gac gtg 240  
 49 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val  
 50 65 70 75 80  
 52 gcc gtg gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg gcg ccg 288  
 53 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro  
 54 85 90 95  
 56 agc cgg agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt 336  
 57 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu  
 58 100 105 110  
 60 cag ctc aat ata gta gag atg aaa gat gaa aat gca act tta gat ggc 384  
 61 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly  
 62 115 120 125  
 64 gga gat gtt tta ttc aca ggc aga gaa ttt ttt gtg ggc ctt tcc aaa 432  
 65 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys  
 66 130 135 140  
 68 agg aca aat caa cga ggt gct gaa atc ttg gct gat act ttt aag gac 480

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69 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
70 145 150 155 160
72 tat gca gtc tcc aca gtg cca gtg gca gat ggg ttg cat ttg aag agt 528
73 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
74 165 170 175
76 ttc tgc agc atg gct ggg cct aac ctg atc gca att ggg tct agt gaa 576
77 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
78 180 185 190
80 tct gca cag aag gcc ctt aag atc atg caa cag atg agt gac cac cgc 624
81 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
82 195 200 205
84 tac gac aaa ctc act gtg cct gat gac ata gca gca aac tgt ata tat 672
85 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
86 210 215 220
88 cta aat atc ccc aac aaa ggg cac gtc ttg ctg cac cga acc ccg gaa 720
89 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
90 225 230 235 240
92 gag tat cca gaa agt gca aag gtt tat gag aaa ctg aag gac cat atg 768
93 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
94 245 250 255
96 ctg atc ccc gtg agc atg tct gaa ctg gaa aag gtg gat ggg ctg ctc 816
97 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
98 260 265 270
100 acc tgc tgc tca gtt tta att aac aag aag gta gac tcc tga 858
101 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
102 275 280 285
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 285
107 <212> TYPE: PRT
108 <213> ORGANISM: H. Sapiens
110 <400> SEQUENCE: 2
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112 1 5 10 15
114 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
115 20 25 30
117 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
118 35 40 45
120 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
121 50 55 60
123 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
124 65 70 75 80
126 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
127 85 90 95
129 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
130 100 105 110
132 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
133 115 120 125
135 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
136 130 135 140

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138 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
139 145          150          155          160
141 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
142          165          170          175
144 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
145          180          185          190
147 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
148          195          200          205
150 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
151          210          215          220
153 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
154 225          230          235          240
156 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
157          245          250          255
159 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
160          260          265          270
162 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
163          275          280          285
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 858
169 <212> TYPE: DNA
170 <213> ORGANISM: H. sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (1)..(858)
176 <400> SEQUENCE: 3
177 atg ggg acg ccg ggg gag ggg ctg ggc cgc tgc tcc cat gcc ctg atc 48
178 Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
179 1 5 10 15
181 cgg gga gtc cca gag agc ctg gcg tcg ggg gaa ggt gcg ggg gct ggc 96
182 Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
183 20 25 30
185 ctt ccc gct ctg gat ctg gcc aaa gct caa agg gag cac ggg gtg ctg 144
186 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
187 35 40 45
189 gga ggt aaa ctg agg caa cga ctg ggg cta cag ctg cta gaa ctg cca 192
190 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
191 50 55 60
193 cct gag gag tca ttg ccg ctg gga ccg ctg ctt ggc gac acg gcc gtg 240
194 Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
195 65 70 75 80
197 atc caa ggg gac acg gcc cta atc acg cgg ccc tgg agc ccc gct cgt 288
198 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
199 85 90 95
201 agg cca gag gtc gat gga gtc cgc aaa gcc ctg caa gac ctg ggg ctc 336
202 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
203 100 105 110
205 cga att gtg gaa ata gga gac gag aac gcg acg ctg gat ggc act gac 384
206 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp

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207          115          120          125
209 gtt ctc ttc acc ggc cgg gag ttt ttc gta ggc ctc tcc aaa tgg acc 432
210 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
211          130          135          140
213 aat cac cga gga gct gag atc gtg gcg gac acg ttc cgg gac ttc gcc 480
214 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
215 145          150          155          160
217 gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc 528
218 Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
219          165          170          175
221 ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc 576
222 Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
223          180          185          190
225 caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc 624
226 Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
227          195          200          205
229 tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt 672
230 Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg
231          210          215          220
233 cct ggg ttg cct ggt gtg ccc cct ttc ctc ctg cac cgt gga ggt ggg 720
234 Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
235 225          230          235          240
237 gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc 768
238 Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
239          245          250          255
241 ctg gta cct gtg tcc tgc tca gaa ctg gag aaa gct ggc gcc ggg ctc 816
242 Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
243          260          265          270
245 agc tcc ctc tgc ttg gtg ctc agc aca cgc ccc cac agc tga 858
246 Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
247          275          280          285
250 <210> SEQ ID NO: 4
251 <211> LENGTH: 285
252 <212> TYPE: PRT
253 <213> ORGANISM: H. sapiens
255 <400> SEQUENCE: 4
256 Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
257 1          5          10          15
259 Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
260          20          25          30
262 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
263          35          40          45
265 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
266          50          55          60
268 Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
269 65          70          75          80
271 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
272          85          90          95
274 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu

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275          100          105          110
277 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
278          115          120          125
280 Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
281          130          135          140
283 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
284 145          150          155          160
286 Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
287          165          170          175
289 Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
290          180          185          190
292 Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
293          195          200          205
295 Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg
296          210          215          220
298 Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
299 225          230          235          240
301 Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
302          245          250          255
304 Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
305          260          265          270
307 Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
308          275          280          285
312 <210> SEQ ID NO: 5
313 <211> LENGTH: 777
314 <212> TYPE: DNA
315 <213> ORGANISM: S. coelicolor
317 <220> FEATURE:
318 <221> NAME/KEY: CDS
319 <222> LOCATION: (1)..(777)
321 <400> SEQUENCE: 5
322 gtg ccc agc aag aag gcc ctg gtc cgc cgc ccc agc ccc agg ctc gcc 48
323 Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala
324 1 5 10 15
326 gaa gga ctg gtg aca cac gtc gag cgg gag cag gtc gat cac ggc ctg 96
327 Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
328 20 25 30
330 gcc ctc gaa cag tgg gac gcc tac gtc gag gcc ctc gga gca cac ggc 144
331 Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly
332 35 40 45
334 tgg gag act ctg gag gtg gac ccg gcc gag tac tgt ccg gac tcg gtc 192
335 Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val
336 50 55 60
338 ttc gtc gag gac gcc gtc gtc gtc ttc cgc aac gtc gcg ctg atc acg 240
339 Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr
340 65 70 75 80
342 cgg ccc ggc gcc gag tcg cgg cgc gcg gag acg gcc ggc gtc gag gag 288
343 Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu
344 85 90 95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,733

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:874 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11